

Cys 65	Glu	Glu	Ser	Phe	Val 70	Lys	Ile	Pro	Gly	Glu 75	Lys	Asp	Ser	Val	Ile 80
Cys	Leu	Lys	Gly	Ser 85	Gln	Trp	Ser	Asp	Ile 90	Glu	Glu	Phe	Cys	Asn 95	Arg
Ser	Cys	Glu	Val 100	Pro	Thr	Arg	Leu	Asn 105	Ser	Ala	Ser	Leu	Lys 110	Gln	Pro
Tyr	Ile	Thr 115	Gln	Asn	Tyr	Phe	Pro	Val 120	Gly	Thr	Val	Val 125	Glu	Tyr	Glu
Cys	Arg 130	Pro	Gly	Tyr	Arg	Arg 135	Glu	Pro	Ser	Leu	Ser 140	Pro	Lys	Leu	Thr
Cys 145	Leu	Gln	Asn	Leu	Lys 150	Trp	Ser	Thr	Ala	Val 155	Glu	Phe	Cys	Lys	Lys 160
Lys	Ser	Cys	Pro	Asn 165	Pro	Gly	Glu	Ile	Arg 170	Asn	Gly	Gln	Ile	Asp 175	Val
Pro	Gly	Gly	Ile 180	Leu	Phe	Gly	Ala	Thr 185	Ile	Ser	Phe	Ser	Cys 190	Asn	Thr
Gly	Tyr	Lys 195	Leu	Phe	Gly	Ser	Thr 200	Ser	Ser	Phe	Cys	Leu 205	Ile	Ser	Gly
Ser 210	Ser	Val	Gln	Trp	Ser	Asp 215	Pro	Leu	Pro	Glu	Cys 220	Arg	Glu	Ile	Tyr
Cys 225	Pro	Ala	Pro	Pro	Gln 230	Ile	Asp	Asn	Gly	Ile 235	Ile	Gln	Gly	Glu	Arg 240
Asp	His	Tyr	Gly	Tyr 245	Arg	Gln	Ser	Val	Thr 250	Tyr	Ala	Cys	Asn 255	Lys	Gly
Phe	Thr	Met 260	Ile	Gly	Glu	His	Ser	Ile 265	Tyr	Cys	Thr	Val 270	Asn	Asn	Asp
Glu	Gly	Glu 275	Trp	Ser	Gly	Pro	Pro 280	Pro	Glu	Cys	Arg	Gly 285	Lys	Ser	Leu
Thr 290	Ser	Lys	Val	Pro	Pro	Thr 295	Val	Gln	Lys	Pro	Thr 300	Thr	Val	Asn	Val
Pro 305	Thr	Thr	Glu	Val	Ser 310	Pro	Thr	Ser	Gln	Lys 315	Thr	Thr	Thr	Lys	Thr 320
Thr	Thr	Pro	Asn 325	Ala	Gln	Ala	Thr	Arg	Ser 330	Thr	Pro	Val	Ser	Arg 335	Thr
Thr	Lys	His 340	Phe	His	Glu	Thr	Thr	Pro 345	Asn	Lys	Gly	Ser 350	Gly	Thr	Thr
Ser	Gly	Thr 355	Thr	Arg	Leu	Leu	Ser 360	Gly	His	Thr	Cys	Phe 365	Thr	Leu	Thr
Gly 370	Leu	Leu	Gly	Thr	Leu	Val 375	Thr	Met	Gly	Leu	Leu 380	Thr,			

or wherein said derivative varies from said fragment only by the substitution of 1 or 2 amino acids.

5. (Thrice amended) A composition according to claim 1 wherein the fragment or derivative includes part or all of the amino acid sequence consisting of amino acids 97-159 of the sequence shown in claim 1.
6. (Thrice amended) A composition according to claim 5 wherein the fragment or derivative includes a sequence having at least five amino acids identical with corresponding amino acids of a contiguous stretch of seven amino acids contained within amino acids 121-128 or 151-158 of the sequence shown in claim 1.
7. (Thrice amended) A composition according to claim 1 wherein the fragment or derivative includes a sequence having at least six amino acids identical with corresponding amino acids of a contiguous stretch of nine amino acids contained within amino acids 83-93 of the sequence shown in claim 1.
11. (Amended) A composition according to claim 1 wherein the fragment is of at least nine contiguous amino acids.
12. (Amended) A composition according to claim 11 wherein the fragment is of at least 13 contiguous amino acids.

13. (Thrice amended) A composition comprising a nucleic acid molecule which encodes a fragment or derivative as specified in claim 1.

14. (Twice amended) A composition according to claim 13 having part of the nucleic acid sequence shown below:

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ccgctgggcg tagctgcgac tcggcgggagt cccggcggcg cgtccttggt ctaacccggc 60
gcgcc atg acc gtc gcg cgg ccg agc gtg ccc gcg gcg ctg ccc etc etc 110
ggg gag ctg ccc cgg ctg ctg ctg ctg gtg ctg ttg tgc ctg ccg gcc 158
gtg tgg ggt gac tgt ggc ctt ccc cca gat gta cct aat gcc cag cca 206
gct ttg gaa ggc cgt aca agt ttt ccc gag gat act gta ata acg tac 254
aaa tgt gaa gaa agc ttt gtg aaa att cct ggc gag aag gac tca gtg 302
atc tgc ctt aag ggc agt caa tgg tca gat att gaa gag ttc tgc aat 350
cgt agc tgc gag gtg cca aca agg cta aat tct gca tcc etc aaa cag 398
cct tat atc act cag aat tat ttt cca gtc ggt act gtt gtg gaa tat 446
gag tgc cgt cca ggt tac aga aga gaa cct tct cta tca cca aaa cta 494
act tgc ctt cag aat tta aaa tgg tcc aca gca gtc gaa ttt tgt aaa 542
aag aaa tca tgc cct aat ccg gga gaa ata cga aat ggt cag att gat 590
gta cca ggt ggc ata tta ttt ggt gca acc atc tcc ttc tca tgt aac 638
aca ggg tac aaa tta ttt ggc tcg act tct agt ttt tgt ctt att tca 686
ggc agc tct gtc cag tgg agt gac ccg ttg cca gag tgc aga gaa att 734
tat tgt cca gca cca cca caa att gac aat gga ata att caa ggg gaa 782
cgt gac cat tat gga tat aga cag tct gta acg tat gca tgt aat aaa 830
gga ttc acc atg att gga gag cac tct att tat tgt act gtg aat aat 878
gat gaa gga gag tgg agt ggc cca cca cct gaa tgc aga gga aaa tct 926
cta act tcc aag gtc cca cca aca gtt cag aaa cct acc aca gta aat 974
gtt cca act aca gaa gtc tca cca act tct cag aaa acc acc aca aaa 1022
acc acc aca cca aat gct caa gca aca cgg agt aca cct gtt tcc agg 1070
aca acc aag cat ttt cat gaa aca acc cca aat aaa gga agt gga acc 1118
act tca ggt act acc cgt ctt cta tct ggg cac acg tgt ttc acg ttg 1166
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aca ggt ttg ctt ggg acg cta gta acc atg ggc ttg ctg act tag 1211  
 ccaaagaaga gttaagaaga aaatacacac aagtatacag actgttccta gtttcttaga 1271  
 cttatctgca tattggataa aataaatgca attgtgctct tcatttagga tgctttcatt 1331  
 gtctttaaga tgtgttagga atgtcaacag agcaaggaga aaaaaggcag tcctggaatc 1391  
 acattcttag cacacctaca cctcttgaaa atagaacaac ttgcagaatt gagagtgatt 1451  
 cctttcctaa aagtgtaga aagcatagag atttggtcgt atttagaatg ggatcacgag 1511  
 gaaaagagaa ggaaagtgat tttttccac aagatctgta atgttatttc cacttataaa 1571  
 ggaaataaaa aatgaaaaac attatttgga tatcaaaagc aaataaaaaac ccaattcagt 1631  
 ctcttctaag caaaattgct aaagagagat gaaccacatt ataaagtaat ctttggtgt 1691  
 aaggcatttt catctttcct tcgggttggc aaaatatttt aaaggtaaaa catgctgggtg 1751  
 aaccaggggt gttgatgggtg ataaggagg aatatagaat gaaagactga atcttccttt 1811  
 gttgcacaaa tagagtttgg aaaaagcctg tgaaagggtgt cttctttgac ttaatgtctt 1871  
 taaaagtatc cagagatact acaatattaa cataagaaaa gattatatat tatttctgaa 1931  
 tcgagatgtc catagtcaaa tttgtaaatc ttattctttt gtaatattta tttatattta 1991  
 tttatgacag tgaacattct gattttacat gtaaaacaag aaaagttgaa gaagatatgt 2051  
 gaagaaaaat gtatttttcc taaatagaaa taaatgatcc cattttttgg t 2102

or the nucleic acid sequence shown below:

tttaaacggg ccctctagac tcgagcggcc gctgcccatc ttgtcgtcgt cgctcttgta 60  
 gtcgtgcatg tgggtgggtt ggtgggtggt aaccatgggt gcgggcgcgc actgtgctgg 120  
 atatctgcag aattcgatgg gcgtagctgc gactcggcgg agtcccggcg gcgcgtcctt 180  
 gttctaaccg ggcgcgcc atg acc gtc gcg cgg ccg agc gtg ccc gcg gcg 231  
 ctg ccc ctc ctc ggg gag ctg ccc cgg ctg ctg ctg gtg ctg ttg 279  
 tgc ctg ccg gcc gtg tgg ggt gac tgt ggc ctt ccc cca gat gta cct 327  
 aat gcc cag cca gct ttg gaa ggc cgt aca agt ttt ccc gag gat act 375  
 gta ata acg tac aaa tgt gaa gaa agc ttt gtg aaa att cct ggc gag 423  
 aag gac tca gtg atc tgc ctt aag ggc agt caa tgg tca gat att gaa 471  
 gag ttc tgc aat cgt agc tgc gag gtg cca aca agg cta aat tct gca 519  
 tcc ctc aaa cag cct tat atc act cag aat tat ttt cca gtc ggt act 567  
 gtt gtg gaa tat gag tgc cgt cca ggt tac aga aga gaa cct tct cta 615  
 tca cca aaa cta act tgc ctt cag aat tta aaa tgg tcc aca gca gtc 663  
 gaa ttt tgt aaa aag aaa tca tgc cct aat ccg gga gaa ata cga aat 711

ggt cag att gat gta cca ggt ggc ata tta ttt ggt gca acc atc tcc 759  
 ttc tca tgt aac aca ggg tac aaa tta ttt ggc tcg act tct agt ttt 807  
 tgt ctt att tca ggc agc tct gtc cag tgg agt gac ccg ttg cca gag 855  
 tgc aga gaa att tat tgt cca gca cca cca caa att gac aat gga ata 903  
 att caa ggg gaa cgt gac cat tat gga tat aga cag tct gta acg tat 951  
 gca tgt aat aaa gga ttc acc atg att gga gag cac tct att tat tgt 999  
 act gtg aat aat gat gaa gga gag tgg agt ggc cca cca cct gaa tgc 1047  
 aga gga aaa tct cta act tcc aag gtc cca cca aca gtt cag aaa cct 1095  
 acc aca gta aat gtt cca act aca gaa gtc tca cca act tct cag aaa 1143  
 acc acc aca aaa acc acc aca cca aat gct caa gca aca cgg agt aca 1191  
 cct gtt tcc agg aca acc aag cat ttt cat gaa aca acc cca aat aaa 1239  
 gga agt gga acc act tca ggt act acc cgt ctt cta tct ggg cac acg 1287  
 tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc atg ggc ttg 1335  
 ctg act tag ccaaagaaga gttaagaaga aaatacacac aagtatacag 1384  
 actgttccta gtttcttaga cttatctgca tattggataa aataaatgca attgtgctct 1444  
 tcatttagga tgctttcatt gtctttaaga tgtgttagga atgtcaaca 1493

19. (Amended) A method of treating a patient having cancer, the method comprising administering to the patient a therapeutically effective amount of a composition as defined in claim 1.

34. (Amended) A composition according to claim 1, wherein said T cell epitope is a T cell epitope of said polypeptide of the CD55 family.

Please cancel claims 2, 4, 8-10, 15-17, 20-24, 26-33, 35 and 36 without prejudice.